

TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATATATATTCATCAATC

TAATCAAACATATGGAGAAGAAATCACTAGCTGGCTTATGCTTCCTCTTCTTGGTTCTCTTTGTT

M E K K S L A G L C F L F L V L F V

GCACAAGAAATTATGGTGACAGAAGCCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGAC
E Q E I M V T E A R T C E N L A D K Y R G P

Δ

CATGCTTTAGTGGTTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGTAG

C F S G C D T H C T T K E N A V S G R C R

GGACGACTTCCGCTGCTGGTGTAATAAAGATGTTAAATGGATCTCCTCCAACATCAAGATGTG

D D F R C W C T K R C *

CAAATAGTCTTTATAATAAACTAAATAAATAAAATGCACGCAGTATAGCTACAACTTCATCTA

TTATATGTACTCAATATCGNGCATAACGTATTAGTTATGCACCTTCTATCATATGGAATAAACAT

AATAAGTAATTTTCGTNTCCAAAAAAAAAAAAAAAAAAAAA

FIG. 1

AlfaAFP2 TGTCAAACACACACATAACACATAAGTGACCGTGAGTCATTAAATTTATA
 AlfaAFP1 -----

AlfaAFP2 TATATTCATCAATCTAATCAAACCTATGGAGAAGAAATCACTAGCTGGCTTA
 AlfaAFP1 -----CAGGCTTA
 * * * * *

AlfaAFP2 TGCTTCCTCTTCCTCGTTCTCTTTGTTGAACAAGAAATTATGGTGACCGAG
 AlfaAFP1 TGCTTCCTCTTCCTGGTTCTCTTTGTTGCACAAGAAATTGTGGTGACAGAA
 * * * * *

AlfaAFP2 GCAGCTACTTGTGAGAATTTGGCTAACACATACAGGGGACCATGCTTCGGT
 AlfaAFP1 GCCAGAACATGTGAGAATTTGGCAGATAAATATAGGGGACCATGCTTTAGT
 * * * * *

AlfaAFP2 GGTGTGACTTTTCACTGCAAAACCAAAGAACAACCTTACTTAGCGGXAGGTGC
 AlfaAFP1 GGTGTGACACTCACTGCACAACCAAAGAGAACGCAGTTAGTGGAAGGTGT
 * * * * *

AlfaAFP2 AGGGACGACTTCCGCTGCTGCTGGATCC
 AlfaAFP1 AGGGACGACTTCCGCTGCTGCTGGATCC
 * * * * *

FIG. 3

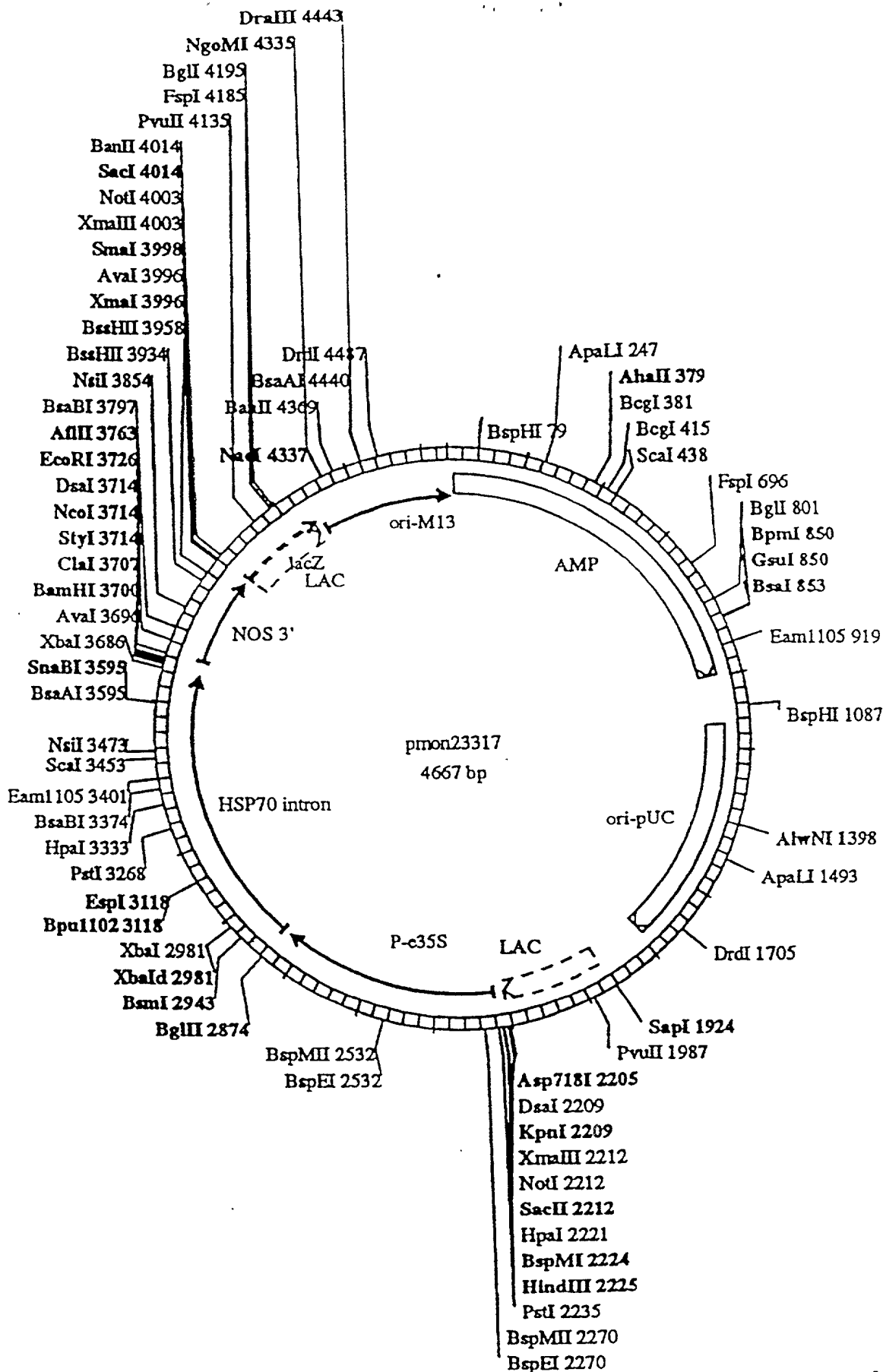


FIG. 4

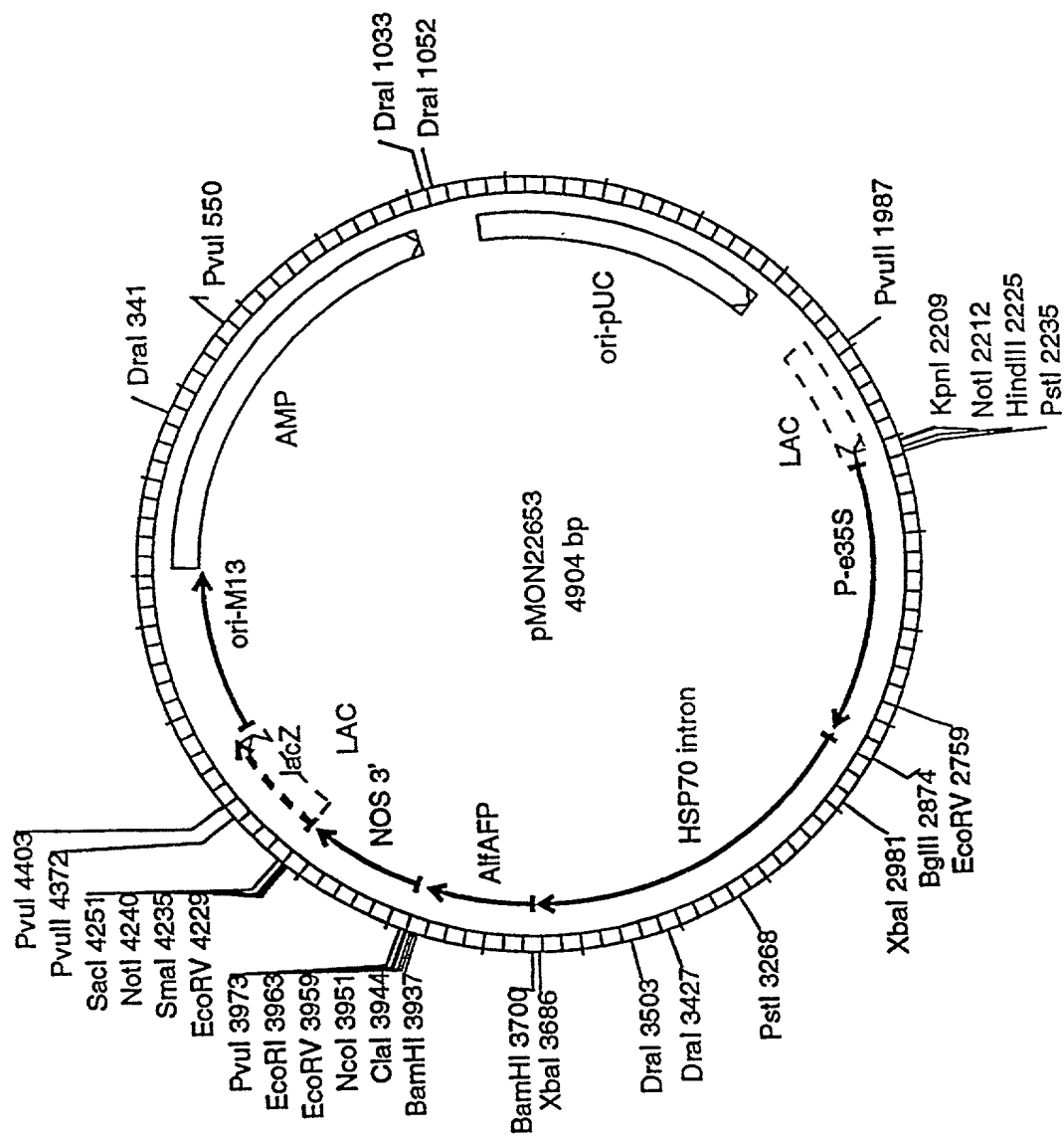


FIG. 5

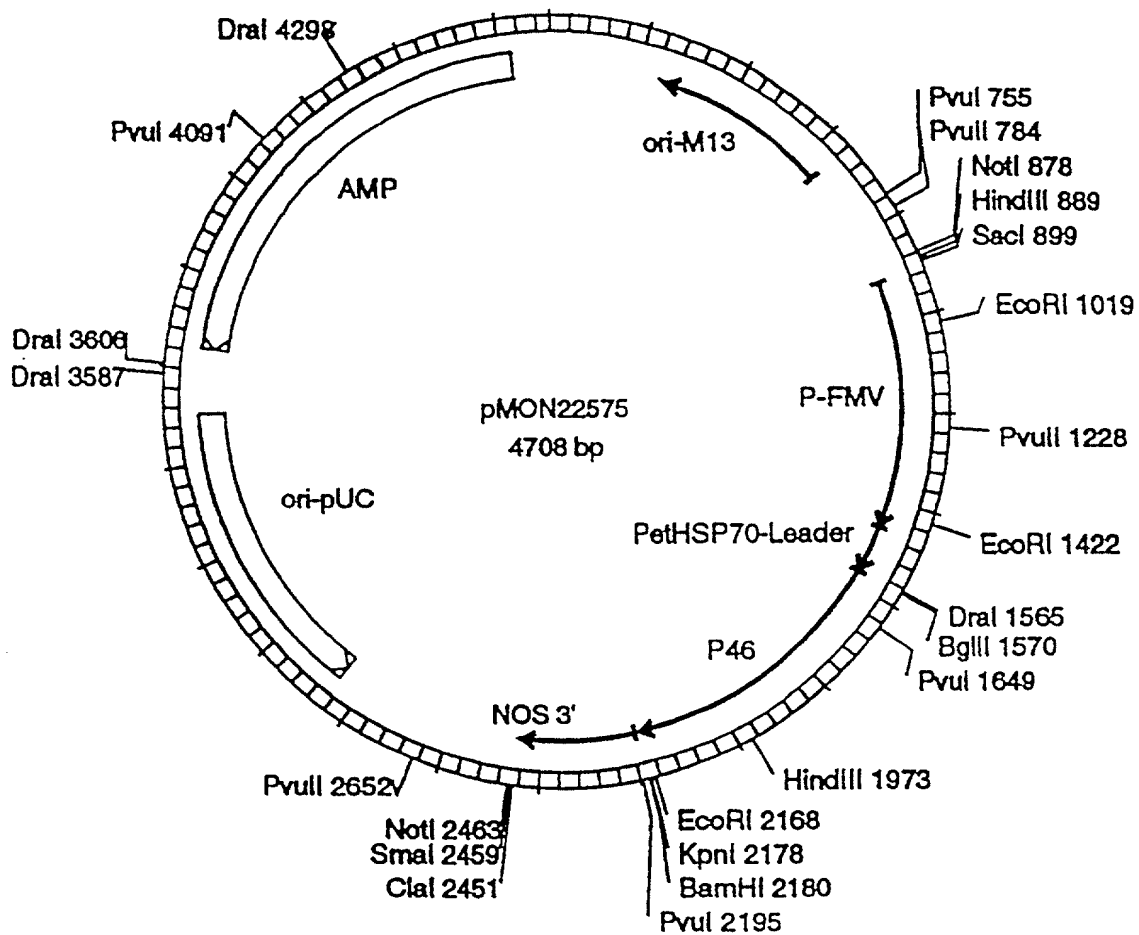


FIG. 6

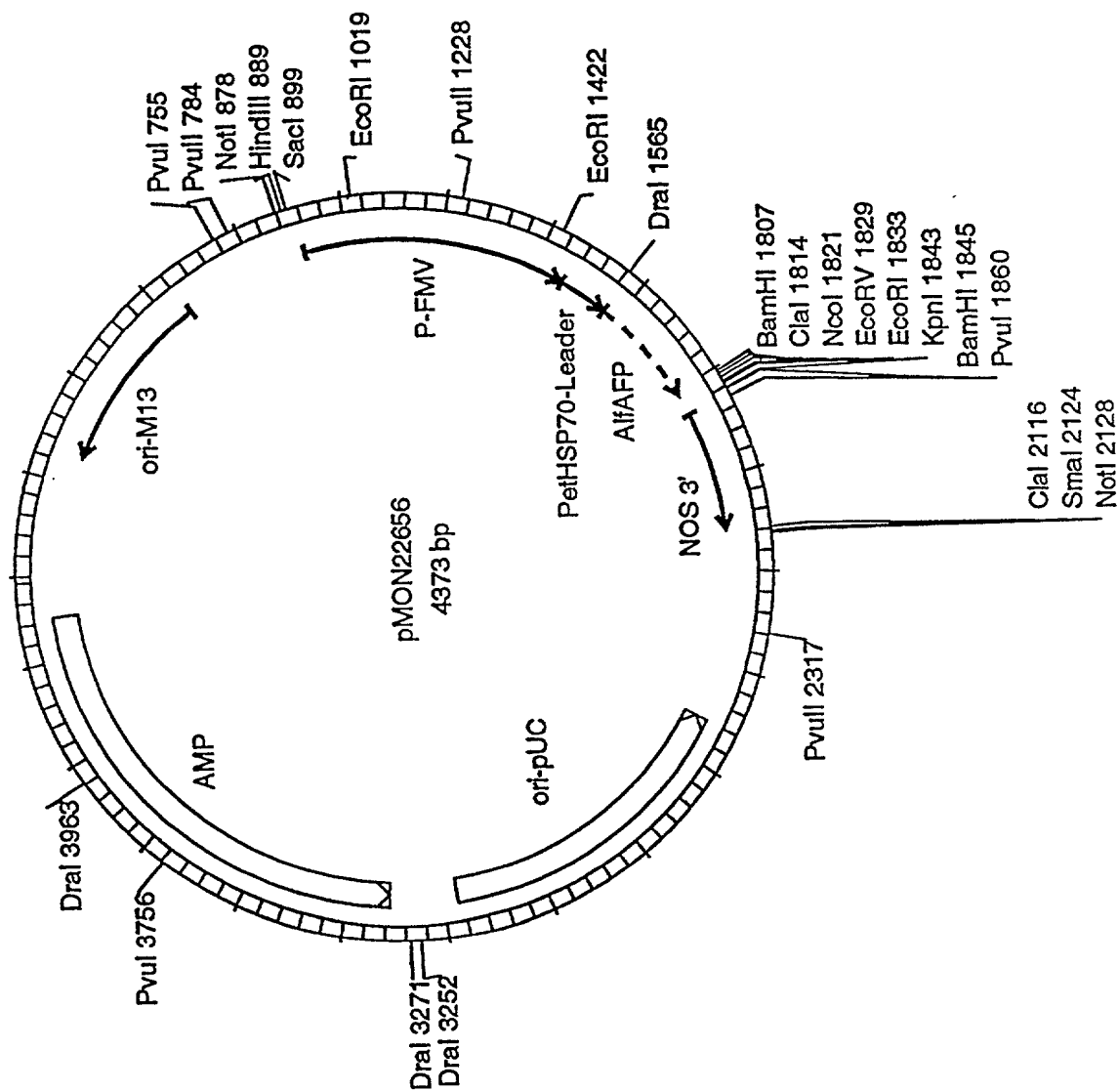


FIG. 7

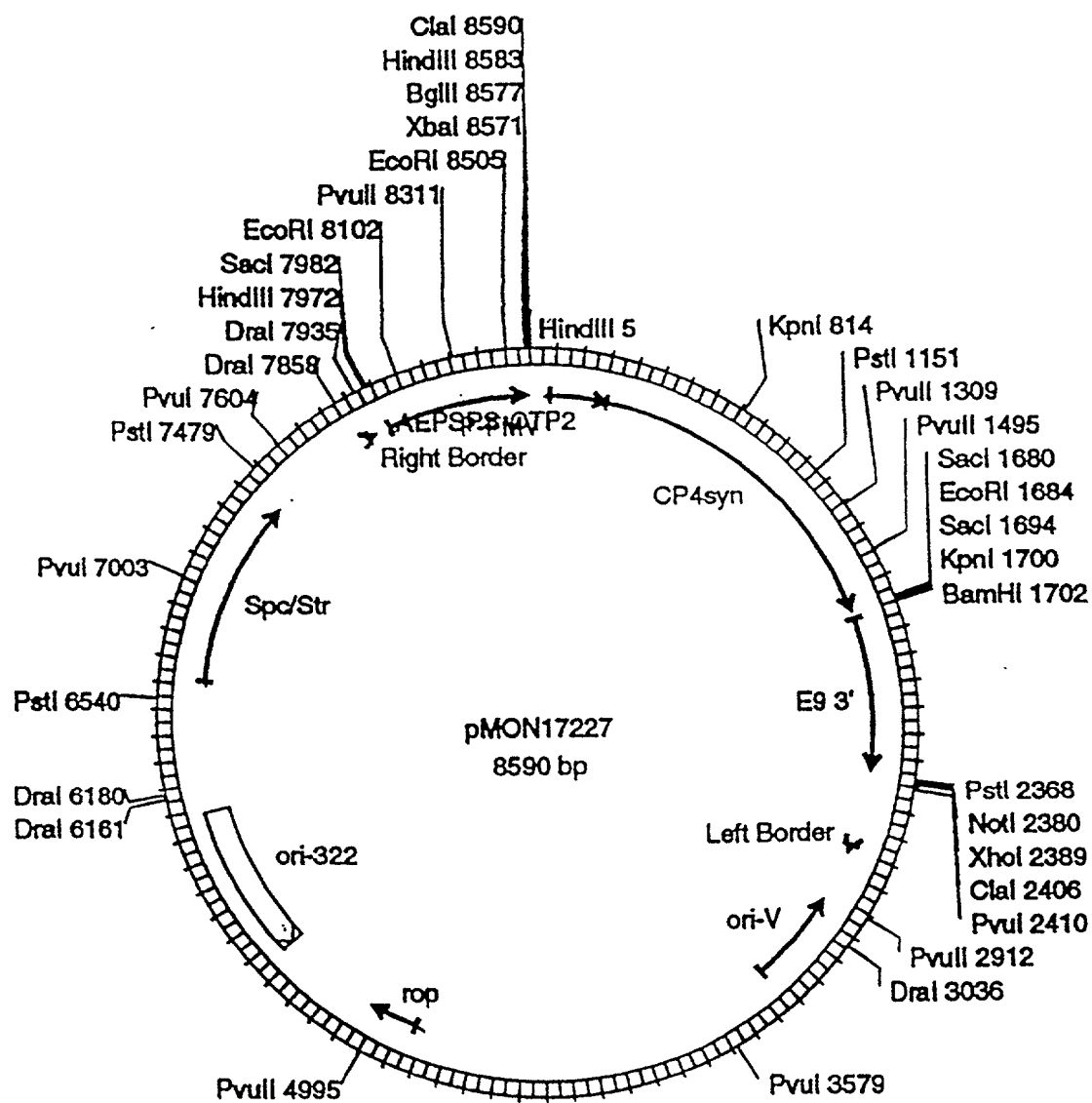


FIG. 8

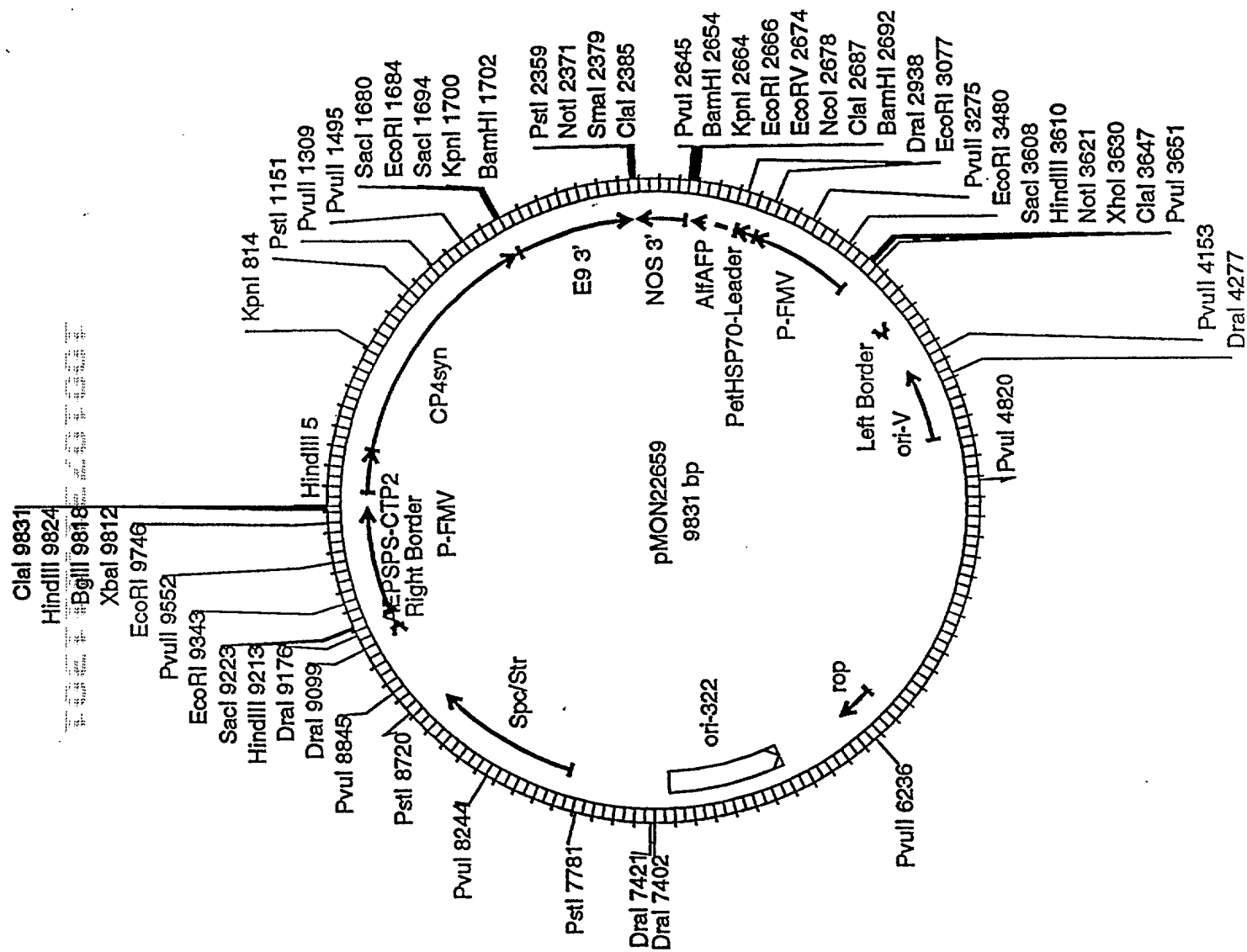


FIG. 9

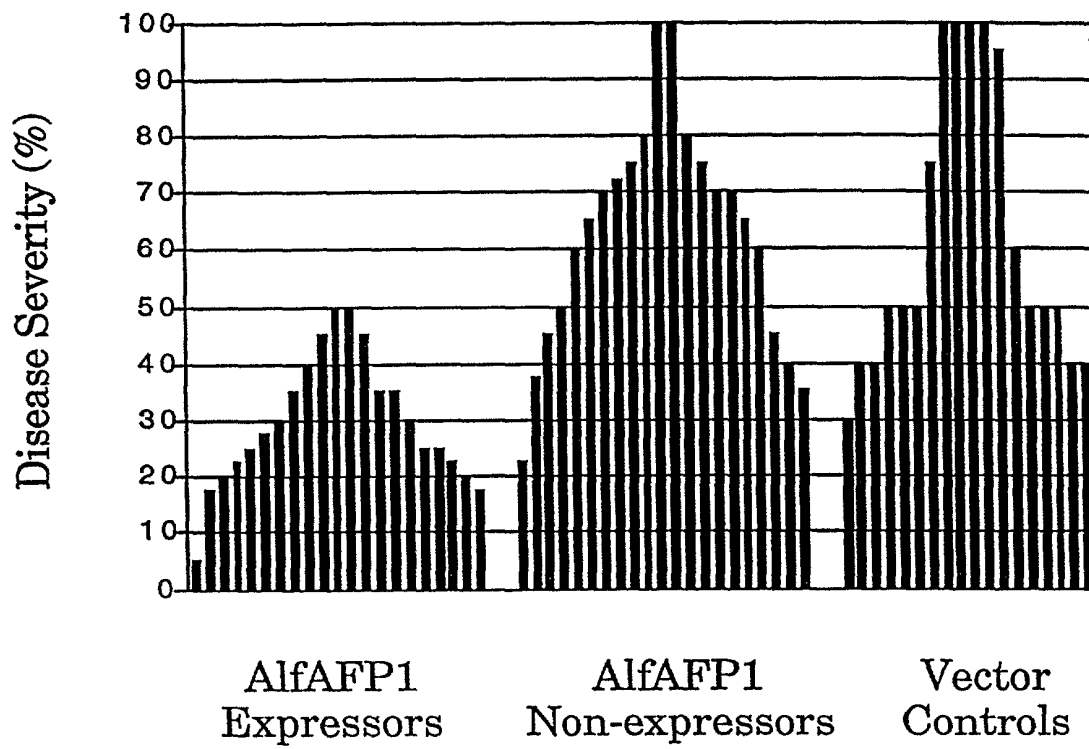


FIG. 10